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Minimum
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Maximum Match 100%
Listing first 45 summaries
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ALIGNMENTS

BB219800 RIKEN full-length enriched, adult male aorta and vein Mus musculus cDNA clone A530057A22 3', mRNA sequence.

BB219800 RIKEN full-length enriched, adult male aorta and vein Mus musculus cDNA clone A530057A22 3', mRNA sequence.

BB219800 SET.

NNSM Mus musculus Eutheria; Rodentia; Craniata; Vertebrata; Euteleostomi; Mus musculus Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus closes 1 to 689)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Jshii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Shiraki, T., Sasaki, D., Shibata, K., Saho, H., Sasaki, D., Shibata, K., Saho, H., Sasaki, D., Shibata, K., Shinagwa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagama, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Wuramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTS (Arakawa, T., et al. 2001)

Unpublished (2001)

To Jun 30, 2000 this sequence version replaced gi:8884753.

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Email: genome-reségsc.riken.go.jp,

URL:http://genome.gsc.riken.go.jp,

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh

Mas 11-1994 Carninci, P., Shibata, Y., Maramatsu, M., Japan Tapid discovery of new genes, Genome Res. . 10 (10), 1617-1630 (2000)

Watshiki, M., Yokoda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, J., Ozawa, K., Tanaka, T., Matsuura

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Encyclopedia Project of Genome Exploration Research Group in Genomic Sciences Center and Genome Science Laboratory in RIKE Division of Experimental Animal Research in Riken contributed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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m FLC} T "
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/dev_stage="adult"
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/clone="A530057A22"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM1911 row: m column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence start: 13
High quality sequence stop: 555
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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603635039F1 NIH_MGC_47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 951)
                                                                                               243
   Conservative
                                                                                               a
                                                                                         /note="organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected > 500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5434545"
/clone_lib="NIH_MGC_47"
                                                                                                                                                                                                                                                                                     /tissue_type="neuroblastoma, cell line"
/lab_host="DH10B (phage-resistant)"
                   52.3%;
Score 362.2;
Pred. No. 7.7e
0; Mismatches
   0;
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                       .7e-
                                         DB 10;
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     Gaps
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JOURNAL
COMMENT
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                                                                                                                                                                                                                                 Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Ko,M., Koya,S., Matsuyama,T., Miyazaki,A., Nome,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sas,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T
Email: genome-res@gsc.riken.go.
URL:http://genome.gsc.riken.go.
Carninci,P., Shibata,Y., Hayats
                                                                     Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
                                                                                                                                                           Muramatsu, M. and Hayashizaki,Y. RIKEN Mouse ESTS (Arakawa,T., e Unpublished (2001)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 697)
                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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                                                        81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           697 bp mRNA linear RIKEN full-length enriched, 12 days embryo,
   Hayatsu, N.,
                                                                                                                                                                                                 et al. 2001)
 Sugahara,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA
 Shibata, K.,
                                                                                                                                              RIKEN Genomic
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                                                                                      230-0045, Japan
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Best Local Similarity
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                                 181 TGCATCACCTGTGCTGTCATCAATCGTGTTCAGAAGGTCAACTGCACAGCTACCTCTAAT
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                                                                                                                                                                              TGTGGTCCTGGACAGGAGCTATCCAAGGATTGTGGTTATGGAGAGGGTGGAGATGCCTAC
                TGCATCACTTGTGCTGTCAATCGGGCCCAGAAGGCCAACTGCACAAATACCTCTAAT
                                                                                      TGCATAGTCTGCCCTCCCGAAAGTATAAAAGCACTTGGGGAACATCACAGATGTCAGACA
                                                                                                                                                             TGTGGCCCTGGACAGGAGCTCTCGAAGGATTGTGGTTATGGAGAAGGTGGAGATGCACAC
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                                                                                                                                                                                                                                                                                                          Conservative
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51.8%; 85.8%;

Score 359.2; Pred. No. 4. Mismatches

359.2; DB 9; No. 4.7e-91; smatches 68;

Indels Length

2

Gaps

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421

361

301

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genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Tanawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Oawa,K., Tanaka,T., Matsuura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizaw,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
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,S., Kawai,J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Computer-based methods for the mouse full-length cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mouse tissues
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prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 370.0 Second
                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="RIKEN full-length enriched, 12 days embryo, embryonic body between diaphragm region and neck" /tissue_type="embryonic body between diaphragm region and
                                                                                                                                                                                                                                                                                 RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5] GAGAGAGAGAGAGCTCCTTTTTTTTTTTTTTTVN 3'], cDNA was
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/clone="9430060M22"
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/lab_host="DH10B"
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Unpublished (2001)
                                                                                                                                                                                                                                                                                        Email: genome resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., It,
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            680 bp mR BB651661 RIKEN full-length enriched, clone C330006C18 5', mRNA sequence. BB651661
                                   Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizav, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                 Hayashizaki,Y.

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Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                          Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Yoshihide Hayashizaki
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Rodentia;
of Full-Length
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d, ES cells Mus musculus cDNA
Mouse cDNAs Compared with
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  BB637179
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musculus
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TGTGGTCCTGGACAGGAGCTATCCAAGGATTGTGGTTATGGAGAGGGTGGAGATGCCTAC 120
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                                                                                                                                                                                                             GCACTGGTGAGCAGCCTGCTAGTGGTGTTTA 451
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e mouse tissues.
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614 bp mRNA linear EST 26-OCT-RIKEN full-length enriched, adult male aorta and vein cDNA clone A530057A22 5', mRNA sequence.
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/clone="C330006C18"
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/strain="C57BL/6J"
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
.M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
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.S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
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Tel: 81-45-503-9222
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                                                                                                                                                                                    prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory
                                                                                                                                          prepared by using trehalose thermo-activated reverse
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subsequently enriched for full-length by went through one round of normalization subtraction to Rot = 459.0. Second
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The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-Tel: 81-45-503-9222
                                                           Laboratory for Genome Exploration Research Sciences Center(GSC), Yokohama Institute
                                                                                                           Contact: Yoshihide Hayashizaki
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                                                                                  Group, RIKEN
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                  230-0045, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCACAGCCTGCCCTCCTCGCAGGTACAAAAGCAGCTGGGGCCACCACAAATGTCAGAGT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTGGCCCTGGACAGGAGCTCTCGAAGGATTGTGGTTATGGAGAAGGTGGAGATGCACAC 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   URL:http://genome.gsc.riken.go.jp/
Carninci.P., Shibata,Y., Hayatsu,M., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                     Mammalia; Eutheria; Rodentia;
1 (bases 1 to 442)
NCI-CGAP http://www.icia.
                   Unpublished (1997)
Other_ESTs: ur48c11.x1
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                                                                                                                                                                                                                                                        BE554624.1 GI:9819111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayashizaki,Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (200)
                                                                                 National Cancer Institute,
                                                                                                       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
                                                                                                                                                                                      Mus musculus
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e mouse tissues
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                                                               Gene Index
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Robert
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cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_line="CCL-142 RAG"
98 c 116 g 10
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/clone="G430003D23"
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Strausberg, Ph.D
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                                                                                                                                                                                                                                                                                                                      442 bp mRNA linear EST 15-AUG-2000 Mus musculus cDNA clone IMAGE:3153524 5',
                                                                                 Cancer Genome Anatomy Project (CGAP),
                                                                                                                                            Craniata; Ver
Sciurognathi;
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                                                                                                                                                                    Vertebrata;
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                                                                                                                                              Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TGCACAGCCTGCCTCCTCGCAGGTACAAAAGCAGCTGGGGGCCACCACAAATGTCAGAGT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 TGTGGCCCTGGACAGGAGCTCTCGAAGGATTGTGGTTATGGAGAAGGTGGAGATGCACAC 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATGGATTGCCAAGAAAATGAGTACTGGGACCAATGGGGACGGTGTCTCACCTGCCAACGG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTGGTCCTGGACAGGAGCTATCCAAGGATTGTGGTTATGGAGAGGGTGGAGATGCCTAC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212;
                                                                                                                                                                                                                                                                                                                                                                                   BB663265 RIKEN full-length enriched, 15 musculus cDNA clone D930037D22 5', mRNA BB663265
                                   Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
                                                                                                                                     Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
                                                                                                                                                                                                                                                                                                                                                    EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Sciences Center(GSC),
Laboratory for Genome Exploration Research Sciences Center(GSC), Yokohama Institute
                                                                                                                                                                                                                                                                   Mammalia;
                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                     BB663265.1 GI:16497019
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Location/Qualifiers
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Site_2: NotI; Cloned unidirectionally. Primer: Olic
Library constructed by Life Technologies. Investigation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              providing samples: Gilbert Smith, NIH" 104\ c 114\ g 101\ t
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/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="IMAGE:3153524"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/strain="FVB/N-3"
                                                                                                                                                                                                                                                                 ; Metazoa; Chordata;
Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.5%;
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Pred. No. 2.4e-37;
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s. Investigator
                     RIKEN Genomic
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Institute of Physical and Chemical Research (RIKEN)

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                                                                                                          253 GATTGCAGGCAGCAGGAATTCAAGGATCGATCTGGAAACTGTGTCCTCTGCAAACAGTGC
                          64 GGTCCTGGACAGGAGCTATCCAAGGATTGTGGTTATGGAGAGGGTGGAGATGCCTACTGC
                                                                                                                                           4 GATTGCCAAGAAATGAGTACTGGGACCAATGGGGACGGTGTGTCACCTGCCAACGGTGT
GGACCTGGCATGGAGTTGTCCAAGGAATGTGGCTTCGGCTATGGGGAGGATGCACAGTGT
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Computer-based methods for the mouse full-length cDNA
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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                                                                                                                                                                                                                           Similarity 59.
49; Conservative
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e mouse tissues
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URL:http://genome.gsc.riken.go.jp/
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URL:http://genome.gsc.riken.go.jp/
Carnlnci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., I
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
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Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsu
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
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Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
D., Shibata,K., Shiragawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
Muramatsu,M. and Hayashizaki,Y.
Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTS (Arakawa,T., et al. 2001)
                                                                                                                                                                              sequencing pipeline with 10 (11), 1757-1771 (2000) Konno, H., Fukunishi, Υ.,
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                                             encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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,K., Fukuda,S.,
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                                                                                                                                               ATGGAGTGTGNGCCCTGCGGAGACCCACCTCCTCCCTACGAACCACACTGTACCCAGCAG
                                                                                                                                                                        CAAGAGTGCATCCCGTGCACGAAGCAGACCCCCCACCTCTGAGGTTCAATGTGCCTTCCAG
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219; Conserv
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BE306459.1
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further details.
e mouse tissues.
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                                                  mRNA sequence.
                                                                601103459F1 NCI_CGAP_Lu29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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/lab_host="DH10B"
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4 GATTGCCAAGAAAATGAGTACTGGGGACCAATGGGGACGGTGTCACCTGCCAACGGTGT 63
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                                                                                                                                                                                                                                                         CAAGAGTGCATCCCGTGCACGAAGCAGACCCCCACCTCTGAGGTTCAATGTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACAGCCTGCCTCCTCGCAGGTACAAAAGCAGCTGGGGCCACCACAAATGTCAGAGTTGC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGACCTGGCATGGAGTTGTCCAAGGAATGTGGCTTCGGCTATGGGGAGGATGCACAGTGT 161
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                                                                                                                                                                                                                                                                                                      ATCACCTGTGCTGTCATCATCGTGTTCAGAAGGTCAACTGCACAGCTACCTCTAATGCT 243
                                                                  BJ004238 F01SSA cDNA Oryzias
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Rodentia; So
1 (bases 1 to 395)
NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, M
BJ004238
BJ004238.1 GI:17355749
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Location/Qualifiers
                                               mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="spontaneous
Stem cell origin."
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="CZECH II (feral)"
/db_xref="taxon:10090"
/clone="IMAGE:3495566"
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                                                                       latipes
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les 216; Conserv
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                                                                                                                                                                                          GTCAACCTGGTG 571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryzias latipes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                   BF162288 894 bp 601770986F1 NCI_CGAP_Lu29 Mus mv
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 Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                               EST
                                                                        mRNA sequence.
BF162288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kohara,Y., Shin-i,T., Kimura,T., Namedaka EST Project in Takeda's lab
                                house mouse.
                                                             BF162288.1 GI:11042496
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81-559-81-6855
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/tissue_type="whole embryo"
/dev_stage="segmentation stage 20
165 c 183 g 118 t
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/strain="Hd-rR"
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Pred. No. 6.7e-24;
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BI919139
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National Institutes of Health, Mammalian
Unpublished (1999)
Homo sapiens
Eukaryota; M
                                                          в1919139.1
                                                                                                                 в1919139
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                            human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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/clone="IMAGE:3990285"
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                          GI:16200214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo of Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

250 c 258 g 209 t
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ll origin."
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Pred. No. 2.1e-20;
0; Mismatches 156;
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ar EST 16-OCT-2001
IMAGE:5248745 5',
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Primer: Oligo dT
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Imotani, K., Ishii

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RESULT 14
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                         BB857078 FIXEN full-length enriched, B16 F10Y cells cDNA clone G370041G09 5', mRNA sequence.
BB857078.1 GI:17098532
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Tissue Procurement: Life Technologies,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cloning). A 0.7-3.5 kb.
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_121"
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1 to 932)
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s is a NIH_MGC Library."
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Pred. No. 1.3e-17;
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                                          124 ACAGCCTGCCCTCCTCGCAGGTACAAAAGCAGCTGGGGCCACCACAAATGTCAGAGTTGC 183
                                                                                                                        302
           361 GTGCCCTGCAGGCCGCACCGGTTAAGGAAGA-CTGGGGGTTTCCAGAAGTGTAAGCCATGT
                                                                                                                                                                                                                           242 GATTGCAGGCAGCAGGAATTCAAGGATCGATCTGGAAACTGTGTCCTCTGCAAACAGTGC 301
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                                                                                                                     GGACCTGGCATGGAGTTGT-CAAGGAATGTGGCTTCGGCTATGGGGAGGATGCACAGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details. e mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,M., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y. RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayashizaki,Y.
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Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ish, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.
                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2001)
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/cell_type="B16 F10Y cells"
138 c 167 g 102 t
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/clone="G370041G09"
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                                                                                                       64
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ACAGCCTGCCTCGCAGGTACAAAAGCAGCTGGGGCCACCACAAATGTCAGAGTTGC
                                                                                  GGTCCTGGACAGGAGCTATCCAAGGATTGTGGTTATGGAGAGGGTGGAGATGCCTACTGC 123
                                                                                                                                        GACTGTGGACAGCAGGAATTCAGGGACCAGTCAGGAAGCTGTGTTCTGTGCAAGCAGTGT 348
                                                                                                                                                              GATTGCCAAGAAAATGAGTACTGGGACCAATGGGGACGGTGTGTCACCTGCCAACGGTGT 63
                                                         GGGCCAGGCATGGAGTTGTCCAAGGAATGTGGCTTTGGCTACGGGGAGGACGCCCAGTGT 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BACKWARD: GTTTTCCCAGTCACGACG
Plate: 65 row: C column: 2
Seq primer: ATTTAGGTGACACTATAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Smith TPL
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adrenal, and endometrium."
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